



032301.232.seq.ST25.txt
SEQUENCE LISTING

<110> Farwick, Mike, et al.

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dep67 GENE

<130> 032301 WD 232

<140> 4

<170> PatentIn version 3.1

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<211> 1756

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<213> Corynebacterium glutamicum

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cagatgggtgc aagtagctgt gaaatgaggg gtaggggcgcg gacgcgttcc agagaaagtg 180

caggtataac cctataata cctgaatctt cctcgtcttc cgcgcctggt ctcaacacct 240

gggtacataa taggagcgt atc gga aaa cat gag gtt gtt gag cac aag gtt 291
Met Gly Lys His Glu Val Ala Gln Gln Thr Val
1 5 10

cgg ggt cct tgg cgg gaa atg gaa gcg cag cgg cgt aaa gag ttg cgg 339
Pro Gly Pro Ser Pro Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg
15 20 25

aag cac aag gcc att gcc act ggc ctg ttg att ttt gct gcc gct gta 387
Lys His Lys Lys Ala Ile Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val
30 35 40

tat ttt att tgc cgt ttc gtc gag acc cgt cgg ggt gaa act gca gcg 435
Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala
45 50 55

tgg gta cgt ttt gtc cgc gct ggc gca gag gcc gga atg att ggc ggg 483
Trp Val Gly Phe Val Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly
60 65 70 75

tat tgc tat tgc ttt ggc gtc acc ggc ctg ttc cgt cat gca ttc tgc 531
Leu Ala Asp Thr Phe Ala Val Thr Ala Leu Ile Arg His Ile Leu Thr
80 85 90

cgc cct att cgt cac act ggc att atc cgg cgc aag aaa gat cag tta 579
Leu Pro Ile Pro His Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu
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gag tgg ctc gcc cag cgg gaa aac ggg gag aaa gtt tgg cgc gaa gtc Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val 140 145 150 155	723
ggc aaa ttg acc gct aat att gtg cgc gca atc gat cgg tca gat gct Gly Lys Leu Thr Ala Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala 160 165 170	771
gaa gag gtg att aaa tct ggg atg atc gac aag att cgg gaa ccc acc Glu Ala Val Ile Lys Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr 175 180 185	819
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aag cgg aac cag ttg tcc agt aac tgg cgc agt ggc tgc aca aaa agt Lys Pro Asn Gln Leu Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg 205 210 215	915
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335

340

345

aga ttg att gtc gar gac tcc ctc cgg cat tca ctc gar acc cgg att 1347
 Arg Leu Leu Val Asp Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile
 335 345 350

acc gga ggc ggt ggt ttc ctc gcc gac aat tac gcc gcc gaa gtc acc 1390
 Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr
 355 360 365

ggc att atc ttc gaa tcc att gaa gga tgg acc att gac gac gtc ttc 1447
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aat gcc acc att gta ggt gca tta gca gga ctg acc att tac gac att 1539
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 Ser His Ile Leu Phe Gly Ala
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 35 40 45 50

Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
 55 60 65

Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe

65

70

75

8

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Ser Ile Pro His
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Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
100 105 110

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
115 120 125

Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
130 135 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
145 150 155 160

Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
165 170 175

Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
180 185 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala Lys Pro Asn Gln Leu
195 200 205

Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg Arg Trp Ala Pro Glu
210 215 220

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
225 230 235 240

Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
245 250 255

Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
260 265 270

Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
275 280 285

Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
290 295 300

Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Thr Ala Ser Ala Ser
 305 310 315 320

800 Sat Sun Aug 816 Sat Sun 800 Thu Aug 816 Thu Aug 816 Fri Aug 816
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Pro Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
370 375 380

Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys His Glu Leu
385 390 395 400

Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
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